AMENDMENTS TO THE CLAIMS

This listing of claims replaces all prior versions, and listings, of claims in the present application.

IN THE CLAIMS:

1. (Previously Presented) A method for prognostication of the development of neoplasia and providing guidance for treatment in a human patient having a neoplasia comprising:

a) determining a nucleotide sequence of exons 2-11 of a cancer-related p53 nucleic acid derived from a human neoplastic tissue or body fluid;

b) analyzing the nucleotide sequence determined in step a) for the presence of mutations; and

c) classifying the neoplasia into different subgroups depending on

(i) the presence or absence of a mutation, and

(ii) whether the patient is node positive or not; and

d) prognosticating the development of the neoplasia by combining the results of steps c)(i) and c)(ii) wherein said results are indicative of patient survival and providing guidance for the treatment of the patient.

2. (Previously Presented) The method of claim 1, further comprising the step of typing the mutation of step c)(ii) into a group selected from the group consisting of a missense mutation, a nonsense mutation, a deletion, and an insertion.

3. (Currently Amended) The method of claim 2, further comprising determining the presence, position, and type of mutation and categorizing biological aggressiveness and/or metastatic potential of the neoplasia based upon the presence, position, and type of mutation,

wherein said neoplasia is breast cancer,

and wherein a frameshift or nonsense mutation in a conserved region II and V of p53 is indicative of poor patient outcome whereas a missense mutation in a conserved region III and IV is indicative of positive patient outcome.

4. (Currently Amended) The method of claim 1 wherein ~~a~~ an exon or exons of the sequenced nucleic acid encode a DNA binding domain.

5. (Previously Presented) The method of claim 1 wherein evolutionary conserved regions of the nucleic acid are analyzed.

6. (Previously Presented) The method of claim 1, wherein the neoplasia is a breast, lung, prostate, gastric, colorectal, melanoma or leukemia neoplasia.

7. (Previously Presented) The method of claim 6, wherein said neoplasia originates from a breast neoplasia.

8. (Previously Presented) The method of claim 7, wherein the detection of the presence of a p53 mutation in a node negative patient tumour sample is indicative of the need of adjuvant therapy following surgical removal of the tumour.

9. (Previously Presented) The method of claim 8, wherein the adjuvant therapy is radiation or chemotherapy/hormone therapy.

10. (Previously Presented) The method of claim 1, wherein step a) is carried out using an automated nucleic acid sequencer, computer software optionally being used to (i) track samples and control process steps and/or (ii) to aid in and/or interpret sequence data obtained.

11. (Canceled).

12. (Canceled).

13. (Canceled).

14. (Previously Presented) A method for prognostication of the development of neoplasia in a human patient having a neoplasia comprising:

a) determining the nucleotide sequence of exons 2-11 of a cancer-related p53 nucleic acid derived from a human neoplastic tissue or body fluid;

b) analyzing the nucleotide sequence determined in step a) for the presence of mutations; and

c) classifying the neoplasia into different subgroups depending on

(i) the presence or absence of a mutation, and

(ii) whether the patient is node positive or not; and

d) prognosticating the development of the neoplasia by combining the results of steps c)(i) and c)(ii), wherein said results are indicative of patient survival.

15. (Previously Presented) A method for prognostication of the development of neoplasia in a human patient having a neoplasia comprising:

a) determining the nucleotide sequence of exons 2-11 of a cancer-related p53 nucleic acid derived from a human neoplastic tissue or body fluid;

b) analyzing the entire nucleotide sequence determined in step a) for the presence of mutations; and

c) classifying the neoplasia into different subgroups depending on the presence or absence of a mutation; and

d) prognosticating the development of the neoplasia by analyzing the results of step c) only, wherein said results are indicative of patient survival.